

Applicant : Christian Fritz et al.  
Serial No. : 10/068,080  
Filed : February 5, 2002  
Page : 2 of 6



Attorney's Docket No.: 15132-090002 / MPI1997-048P1R2DV1

RECEIVED  
JUN 09 2003

In the Specification:

Please amend the paragraph beginning at page 1, line 5 as follows:

TFCH CENTER 1600/2900

B) This application is a divisional of U.S. Patent Application Serial No. 09/163,445, filed on September 30, 1998 (now U.S. Patent No. 6,472,377), which claims priority from U.S. Provisional Application Serial No. 60/070,116, filed on December 31, 1997, both of which are incorporated herein by reference in their entirety.

Please amend the paragraph beginning at page 14, line 9, as follows:

B<sup>2</sup> The determination of percent identity or homology between two sequences can be accomplished using a mathematical algorithm. A suitable, mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Nat'l Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Nat'l Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to yneS nucleic acid molecules described herein. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to yneS protein molecules. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See the National Institute of Health website at address: World Wide Web ([www](http://www.ncbi.nlm.nih.gov)) [ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov) ~~http://www.ncbi.nlm.nih.gov~~. Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used.